

NRSEs present in neuronal genes			Intragenic Position
NRSEs present in neuronal genes	Consensus	Sequence	
CONSENSUS:	TTCAGCACCCnCGGAGAGnGCC		
SOG10	GCCAT	-----T-----	5' UTR
Na CHANNEL	TGGGT	-----A-----	5' UTR
SYNAPSIN I	CCAGC	-----C-----	5' UTR
BDNF	GTCCA	-----T-----	5' UTR
GLYCINE RECEPT (rev)	GGGT	-----T-----	5' UTR
NMDA RECEPTOR	CCCGC	-----	5' UTR
ACH RECEPTOR B2	GCGGC	-----	5' UTR
NEUROFILIMANE-M	GGGT	-----T-----	5' UTR
B-4 TUBULIN	CGCCG	-----	5' UTR
CORT. RELEASING FCTR	GGCGC	-----	5' UTR
CALBINDIN	GCACA	-----	5' UTR
SYNAPTOTAGMIN-4	GTTCT	-----A-----	5' UTR
HES-3	GGCA	-----	5' UTR
SYNAPTOPHYSIN	CGGCG	-----T-----	5' UTR

FIG. 1A

Evolutionary conservation of NRSEs			Intragenic Position
Gene	Consensus	Sequence	
HUMAN CALBINDIN	AG	-----A-----	5' UTR
CHICKEN CALBINDIN	G	-----	5' UTR
RAT CALBINDIN	AG	-----	5' UTR
MOUSE CALBINDIN	AG	-----	5' UTR
HUMAN CRF:			
RAT CRF		-----	5' UTR
SHEEP CRF		-----T-----	5' UTR
XENOPUS CRF		-----AA-----	5' UTR
HUMAN NEURONAL NIC ACHR B-2		-----	5' UTR
RAT NEURONAL NIC ACHR B-2		-----T-----	5' UTR
HUMAN NMDAR (NR1-1)		-----	5' UTR
RAT NMDAR (NR1-1)		-----AT-----	5' UTR
HUMAN SYNAPSIN I		-----	5' UTR
RAT SYNAPSIN I		-----T-----	5' UTR

FIG. 1B

NRSEs in non-neuronal genes				FIG. 1C			
SOM. ACT. FCTR. (rev)	GTCTCT	-----A	CGCAG	5' UTR			
NCAM	GCGAT	-----AA	CCTGG	1st Intron			
ATRIAL NATRIURETIC PEPTIDE	TAAAC	-----CG-	CGAGG	3' UTR			
RAT APRT (rev)	GCTGA	G-----T	TGACC	Intron			
BOVINE P-450 (rev)	AGTTC	-----G	AGGCT	Intron			
CANINE DISTEMPER VIRUS (rev)	TGTCT	---C-T-----G---	AGAGT	Coding region			
SHEEP KERATIN	ATGTG	A-----G-	ATGAG	5' Regulatory			
MOUSE SKELETAL ACTIN (rev)	GCTTC	GG-----C-----	GCCAG	3' Regulatory			
T-CELL RECEPTOR BETA	GTACC	G-----A-T-----	TGACA	Coding Region			
PIG LACTALBUMIN (rev)	TGTCT	-----G-----T-A	CATTT	Coding Region			

Transcriptional Repression by λ HZ4

Reporter Plasmid	pCMV-HZ4	Percent CAT activity	Fold repression
pCAT3-S36++	0 μ g	100	-
	1	8.3 \pm 0.6	11.4
	4	3.1 \pm 0.3	32
pCAT3	0	100	-
	1	77 \pm 0.8	1.3
	4	67.5 \pm 3.8	1.5

FIG. 2

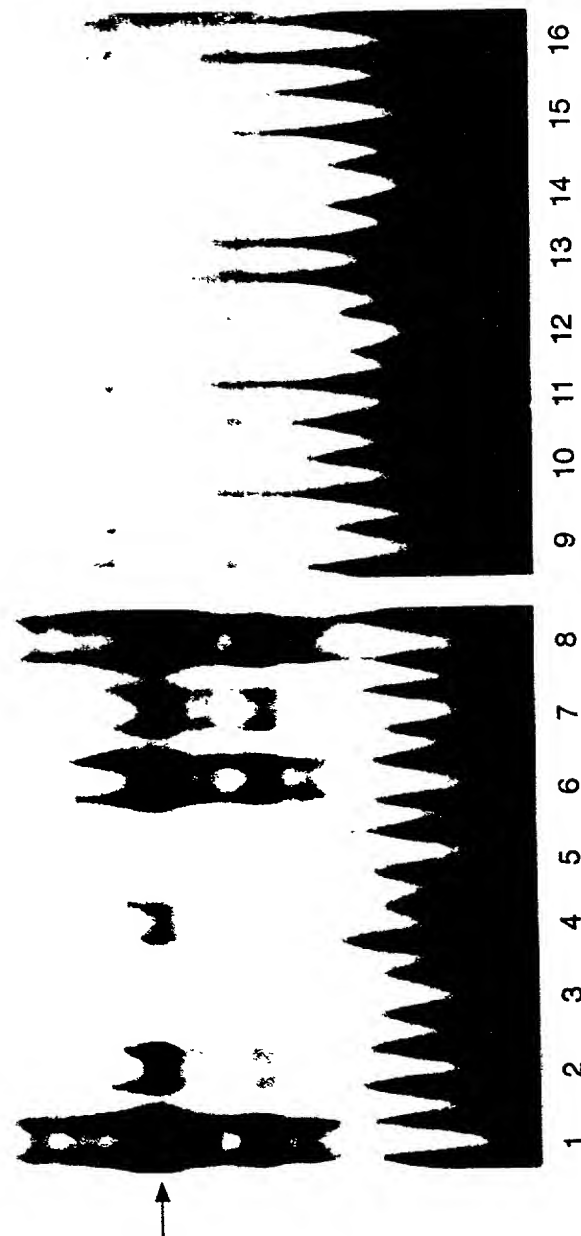


FIG. 3

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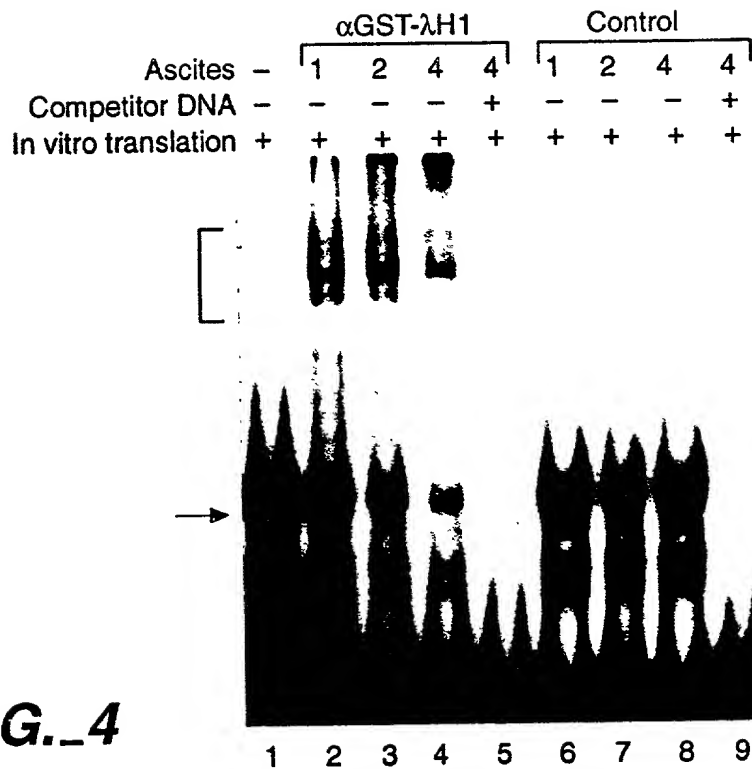
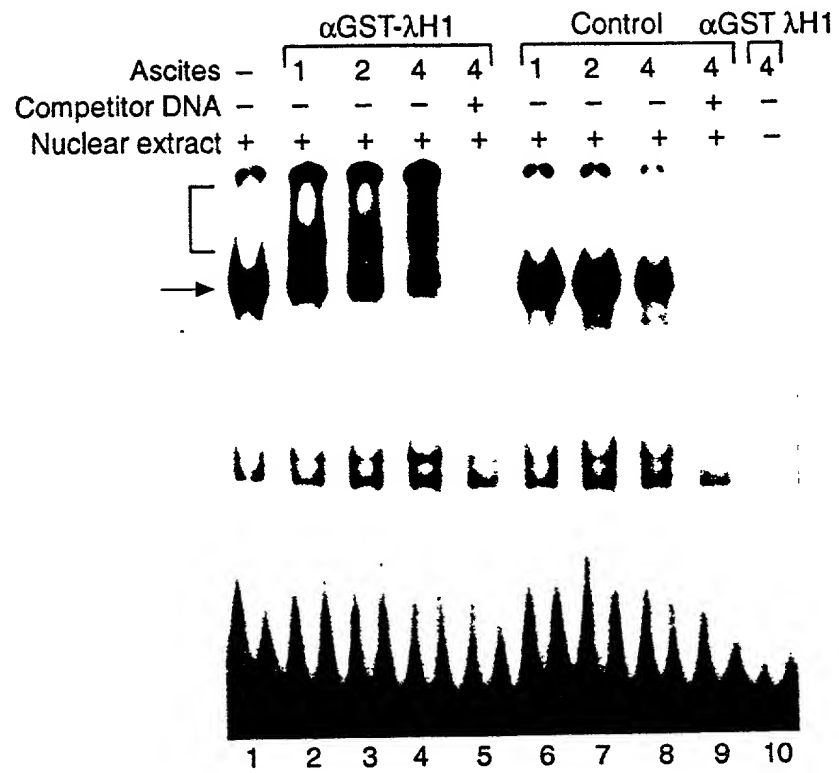
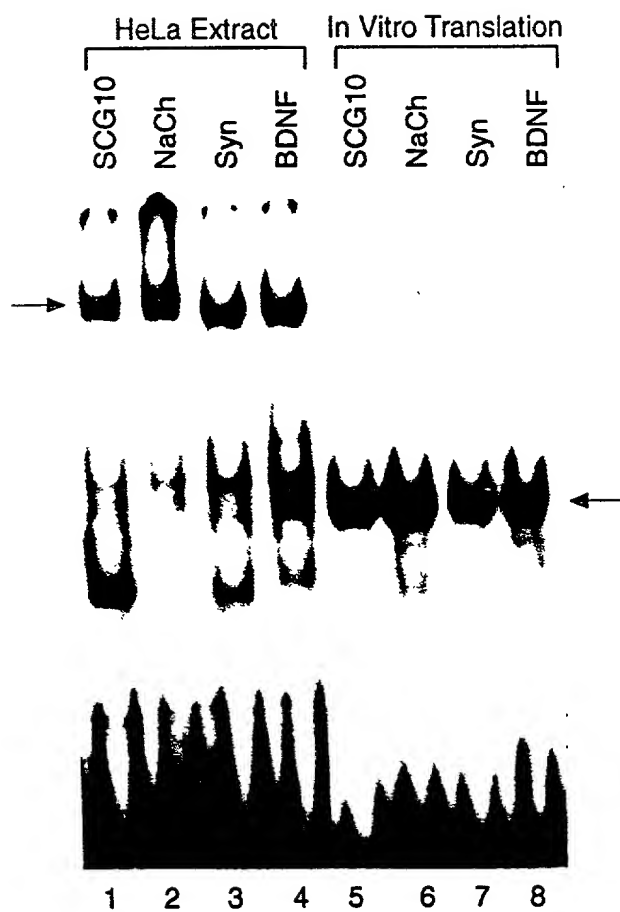


FIG._4

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TOP SECRET

**FIG._5**

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GAATTCC		GGG	GCC	CCA	GAC	CCT	GGC	GGC	GGC	TGC	GGC	AGC	CGA	GAC	GGC	49
		Gly	Ala	Pro	Asp	Pro	Gly	Gly	Gly	Cys	Gly	Ser	Arg	Asp	Gly	
		1				5					10					
AGG	GCG	AGG	CCC	GGA	GGC	CTG	AGC	ACC	CTC	TGC	AGC	CCC	ACT	CCT	GGG	97
Arg	Ala	Arg	Pro	Gly	Gly	Leu	Ser	Thr	Leu	Cys	Ser	Pro	Thr	Pro	Gly	
15				20						25					30	
CCT	TCT	TGG	TCC	ACG	ACG	GCC	CCA	GCA	CCC	AAC	TTT	ACC	ACC	CTC	CCC	145
Pro	Ser	Trp	Ser	Thr	Thr	Ala	Pro	Ala	Pro	Asn	Phe	Thr	Thr	Leu	Pro	
				35					40					45		
CAC	CTC	TCC	CCC	GAA	ACT	CCA	GCA	ACA	AAG	AAA	AGT	AGT	CGG	AGA	AGG	193
His	Leu	Ser	Pro	Glu	Thr	Pro	Ala	Thr	Lys	Lys	Ser	Ser	Arg	Arg	Arg	
			50					55					60			
AGC	GGC	GAC	TCA	GGG	TCG	CCC	GCC	CCT	CCT	CAC	CGA	GGA	AGG	CCG	AAT	241
Ser	Gly	Asp	Ser	Gly	Ser	Pro	Ala	Pro	Pro	His	Arg	Gly	Arg	Pro	Asn	
		65					70					75				
ACA	GTT	ATG	GCC	ACC	CAG	GTA	ATG	GGG	CAG	TCT	TCT	GGA	GGA	GGA	GGG	289
Thr	Val	Met	Ala	Thr	Gln	Val	Met	Gly	Gln	Ser	Ser	Gly	Gly	Gly	Gly	
	80					85					90					
CTG	TTT	ACC	AGC	AGT	GGC	AAC	ATT	GGA	ATG	GCC	CTG	CCT	AAC	GAC	ATG	337
Leu	Phe	Thr	Ser	Ser	Gly	Asn	Ile	Gly	Met	Ala	Leu	Pro	Asn	Asp	Met	
95					100					105					110	
TAT	GAC	TTG	CAT	GAC	CTT	TCC	AAA	GCT	GAA	CTG	GCC	GCA	CCT	CAG	CTT	385
Tyr	Asp	Leu	His	Asp	Leu	Ser	Lys	Ala	Glu	Leu	Ala	Ala	Pro	Gln	Leu	
				115					120					125		
ATT	ATG	CTG	GCA	AAT	GTG	GCC	TTA	ACT	GGG	GAA	GTA	AAT	GGC	AGC	TGC	433
Ile	Met	Leu	Ala	Asn	Val	Ala	Leu	Thr	Gly	Glu	Val	Asn	Gly	Ser	Cys	
			130					135					140			
TGT	GAT	TAC	CTG	GTC	GGT	GAA	GAA	AGA	CAG	ATG	GCA	GAA	CTG	ATG	CCG	481
Cys	Asp	Tyr	Leu	Val	Gly	Glu	Glu	Arg	Gln	Met	Ala	Glu	Leu	Met	Pro	
		145					150					155				
GTT	GGG	GAT	AAC	AAC	TTT	TCA	GAT	AGT	GAA	GAA	GGA	GAA	GGA	CTT	GAA	529
Val	Gly	Asp	Asn	Asn	Phe	Ser	Asp	Ser	Glu	Glu	Gly	Glu	Gly	Leu	Glu	
	160					165					170					
GAG	TCT	GCT	GAT	ATA	AAA	GGT	GAA	CCT	CAT	GGA	CTG	GAA	AAC	ATG	GAA	577
Glu	Ser	Ala	Asp	Ile	Lys	Gly	Glu	Pro	His	Gly	Leu	Glu	Asn	Met	Glu	
175				180						185					190	
CTG	AGA	AGT	TTG	GAA	CTC	AGC	GTC	GTA	GAA	CCT	CAG	CCT	GTA	TTT	GAG	625
Leu	Arg	Ser	Leu	Glu	Leu	Ser	Val	Val	Glu	Pro	Gln	Pro	Val	Phe	Glu	
				195					200					205		
GCA	TCA	GGT	GCT	CCA	GAT	ATT	TAC	AGT	TCA	AAT	AAA	GAT	CTT	CCC	CCT	673
Ala	Ser	Gly	Ala	Pro	Asp	Ile	Tyr	Ser	Ser	Asn	Lys	Asp	Leu	Pro	Pro	
			210					215					220			
GAA	ACA	CCT	GGA	GCG	GAG	GAC	AAA	GGC	AAG	AGC	TCG	AAG	ACC	AAA	CCC	721
Glu	Thr	Pro	Gly	Ala	Glu	Asp	Lys	Gly	Lys	Ser	Ser	Lys	Thr	Lys	Pro	
		225					230					235				

FIG._6A**SUBSTITUTE SHEET (RULE 26)**

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TTT	CGC	TGT	AAG	CCA	TGC	CAA	TAT	GAA	GCA	GAA	TCT	GAA	GAA	CAG	TTT	769
Phe	Arg	Cys	Lys	Pro	Cys	Gln	Tyr	Glu	Ala	Glu	Ser	Glu	Glu	Gln	Phe	
240						245					250					
GTG	CAT	CAC	ATC	AGA	GTT	CAC	AGT	GCT	AAG	AAA	TTT	TTT	GTG	GAA	GAG	817
Val	His	His	Ile	Arg	Val	His	Ser	Ala	Lys	Lys	Phe	Phe	Val	Glu	Glu	
255					260					265					270	
AGT	GCA	GAG	AAG	CAG	GCA	AAA	GCC	AGG	GAA	TCT	GGC	TCT	TCC	ACT	GCA	865
Ser	Ala	Glu	Lys	Gln	Ala	Lys	Ala	Arg	Glu	Ser	Gly	Ser	Ser	Thr	Ala	
				275					280					285		
GAA	GAG	GGA	GAT	TTC	TCC	AAG	GGC	CCC	ATT	CGC	TGT	GAC	CGC	TGC	GGC	913
Glu	Glu	Gly	Asp	Phe	Ser	Lys	Gly	Pro	Ile	Arg	Cys	Asp	Arg	Cys	Gly	
			290					295					300			
TAC	AAT	ACT	AAT	CGA	TAT	GAT	CAC	TAT	ACA	GCA	CAC	CTG	AAA	CAC	CAC	961
Tyr	Asn	Thr	Asn	Arg	Tyr	Asp	His	Tyr	Thr	Ala	His	Leu	Lys	His	His	
	305						310					315				
ACC	AGA	GCT	GGG	GAT	AAT	GAG	CGA	GTC	TAC	AAG	TGT	ATC	ATT	TGC	ACA	1009
Thr	Arg	Ala	Gly	Asp	Asn	Glu	Arg	Val	Tyr	Lys	Cys	Ile	Ile	Cys	Thr	
	320					325					330					
TAC	ACA	ACA	GTG	AGC	GAG	TAT	CAC	TGG	AGG	AAA	CAT	TTA	AGA	AAC	CAT	1057
Tyr	Thr	Thr	Val	Ser	Glu	Tyr	His	Trp	Arg	Lys	His	Leu	Arg	Asn	His	
335					340					345					350	
TTT	CCA	AGG	AAA	GTA	TAC	ACA	TGT	GGA	AAA	TGC	AAC	TAT	TTT	TCA	GAC	1105
Phe	Pro	Arg	Lys	Val	Tyr	Thr	Cys	Gly	Lys	Cys	Asn	Tyr	Phe	Ser	Asp	
			355					360						365		
AGA	AAA	AAC	AAT	TAT	GTT	CAG	CAT	GTT	AGA	ACT	CAT	ACA	GGA	GAA	CGC	1153
Arg	Lys	Asn	Asn	Tyr	Val	Gln	His	Val	Arg	Thr	His	Thr	Gly	Glu	Arg	
			370					375					380			
CCA	TAT	AAA	TGT	GAA	CTT	TGT	CCT	TAC	TCA	AGT	TCT	CAG	AAG	ACT	CAT	1201
Pro	Tyr	Lys	Cys	Glu	Leu	Cys	Pro	Tyr	Ser	Ser	Ser	Gln	Lys	Thr	His	
		385				390						395				
CTA	ACT	AGA	CAT	ATG	CGT	ACT	CAT	TCA	GGT	GAG	AAG	CCA	TTT	AAA	TGT	1249
Leu	Thr	Arg	His	Met	Arg	Thr	His	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys	
	400					405					410					
GAT	CAG	TGC	AGT	TAT	GTG	GCC	TCT	AAT	CAA	CAT	GAA	GTA	ACC	CGC	CAT	1297
Asp	Gln	Cys	Ser	Tyr	Val	Ala	Ser	Asn	Gln	His	Glu	Val	Thr	Arg	His	
415					420					425					430	
GCA	AGA	CAG	GTT	CAC	AAT	GGG	CCT	AAA	CCT	CTT	AAT	TGC	CCA	CAC	TGT	1345
Ala	Arg	Gln	Val	His	Asn	Gly	Pro	Lys	Pro	Leu	Asn	Cys	Pro	His	Cys	
			435					440					445			
GAT	TAC	AAA	ACA	GCA	GAT	AGA	AGC	AAC	TTC	AAA	AAA	CAT	GTA	GAG	CTA	1393
Asp	Tyr	Lys	Thr	Ala	Asp	Arg	Ser	Asn	Phe	Lys	Lys	His	Val	Glu	Leu	
			450					455					460			

FIG. 6B**SUBSTITUTE SHEET (RULE 26)**

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CAT	GTG	AAC	CCA	CGG	CAG	TTC	AAT	TGC	CCT	GTA	TGT	GAC	TAT	GCA	GCT	1441
His	Val	Asn	Pro	Arg	Gln	Phe	Asn	Cys	Pro	Val	Cys	Asp	Tyr	Ala	Ala	
		465					470					475				
TCC	AAG	AAG	TGT	AAT	CTA	CAG	TAT	CAC	TTC	AAA	TCT	AAG	CAT	CCT	ACT	1489
Ser	Lys	Lys	Cys	Asn	Leu	Gln	Tyr	His	Phe	Lys	Ser	Lys	His	Pro	Thr	
	480					485					490					
TGT	CCT	AAT	AAA	ACA	ATG	GAT	GTC	TCA	AAA	GTG	AAA	CTA	AAG	AAA	ACC	1537
Cys	Pro	Asn	Lys	Thr	Met	Asp	Val	Ser	Lys	Val	Lys	Leu	Lys	Lys	Thr	
495					500					505					510	
AAA	AAA	CGA	GAG	GCT	GAC	TTG	CCT	GAT	AAT	ATT	ACC	AAT	GAA	AAA	ACA	1585
Lys	Lys	Arg	Glu	Ala	Asp	Leu	Pro	Asp	Asn	Ile	Thr	Asn	Glu	Lys	Thr	
			515						520					525		
GAA	ATA	GAA	CAA	ACA	AAA	ATA	AAA	GGG	GAT	GTG	GCT	GGA	AAG	AAA	AAT	1633
Glu	Ile	Glu	Gln	Thr	Lys	Ile	Lys	Gly	Asp	Val	Ala	Gly	Lys	Lys	Asn	
			530					535					540			
GAA	AAG	TCC	GTC	AAA	GCA	GAG	AAA	AGA	GAT	GTC	TCA	AAA	GAG	AAA	AAG	1681
Glu	Lys	Ser	Val	Lys	Ala	Glu	Lys	Arg	Asp	Val	Ser	Lys	Glu	Lys	Lys	
		545					550					555				
CCT	TCT	AAT	AAT	GTG	TCA	GTG	ATC	CAG	GTG	ACT	ACC	AGA	ACT	CGA	AAA	1729
Pro	Ser	Asn	Asn	Val	Ser	Val	Ile	Gln	Val	Thr	Thr	Arg	Thr	Arg	Lys	
	560					565					570					
TCA	GTA	ACA	GAG	GTG	AAA	GAG	ATG	GAT	GTG	CAT	ACA	GGA	AGC	AAT	TCA	1777
Ser	Val	Thr	Glu	Val	Lys	Glu	Met	Asp	Val	His	Thr	Gly	Ser	Asn	Ser	
575					580					585					590	
GAA	AAA	TTC	AGT	AAA	ACT	AAG	AAA	AGC	AAA	AGG	AAG	CTG	GAA	GTT	GAC	1825
Glu	Lys	Phe	Ser	Lys	Thr	Lys	Lys	Ser	Lys	Arg	Lys	Leu	Glu	Val	Asp	
			595					600						605		
AGC	CAT	TCT	TTA	CAT	GGT	CCT	GTG	AAT	GAT	GAG	GAA	TCT	TCA	ACA	AAA	1873
Ser	His	Ser	Leu	His	Gly	Pro	Val	Asn	Asp	Glu	Glu	Ser	Ser	Thr	Lys	
			610					615				620				
AAG	AAA	AAG	AAG	GTA	GAA	AGC	AAA	TCC	AAA	AAT	AAT	AGT	CAG	GAA	GTG	1921
Lys	Lys	Lys	Lys	Val	Glu	Ser	Lys	Ser	Lys	Asn	Asn	Ser	Gln	Glu	Val	
		625					630					635				
CCA	AAG	GGT	GAC	AGC	AAA	GTG	GAG	GAG	AAT	AAA	AAG	CAA	AAT	ACT	TGC	1969
Pro	Lys	Gly	Asp	Ser	Lys	Val	Glu	Glu	Asn	Lys	Lys	Gln	Asn	Thr	Cys	
	640					645					650					
ATG	AAA	AAA	AGT	ACA	AAG	AAG	AAA	ACT	CTG	AAA	AAT	AAA	TCA	AGT	AAG	2017
Met	Lys	Lys	Ser	Thr	Lys	Lys	Lys	Thr	Leu	Lys	Asn	Lys	Ser	Ser	Lys	
655					660					665					670	
AAA	AGC	AGT	AAG	CCT	TCT	CGGAATTC										2043
Lys	Ser	Ser	Lys	Pro	Ser											
				675												

FIG. 6C
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FIG. 6C
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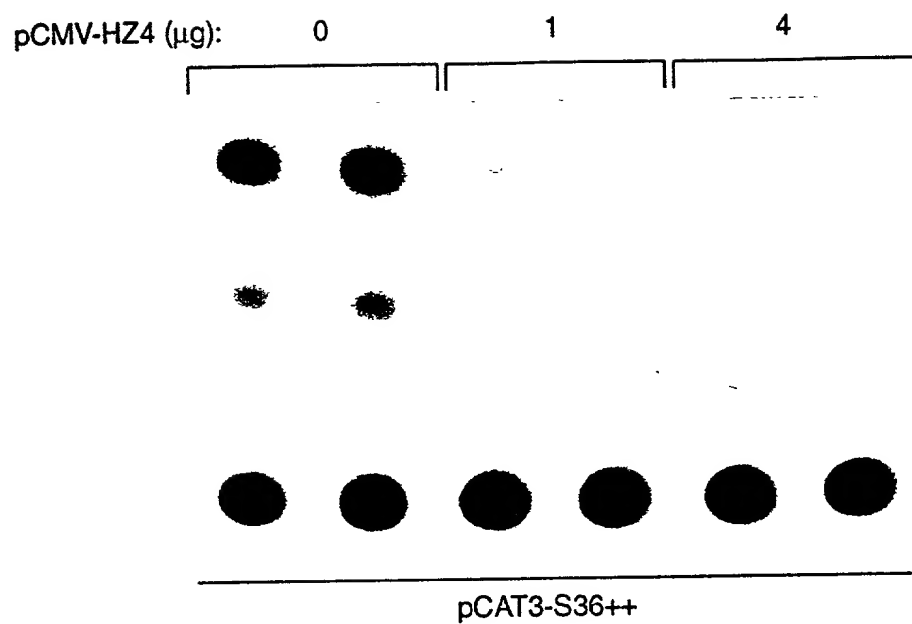


FIG. 8A

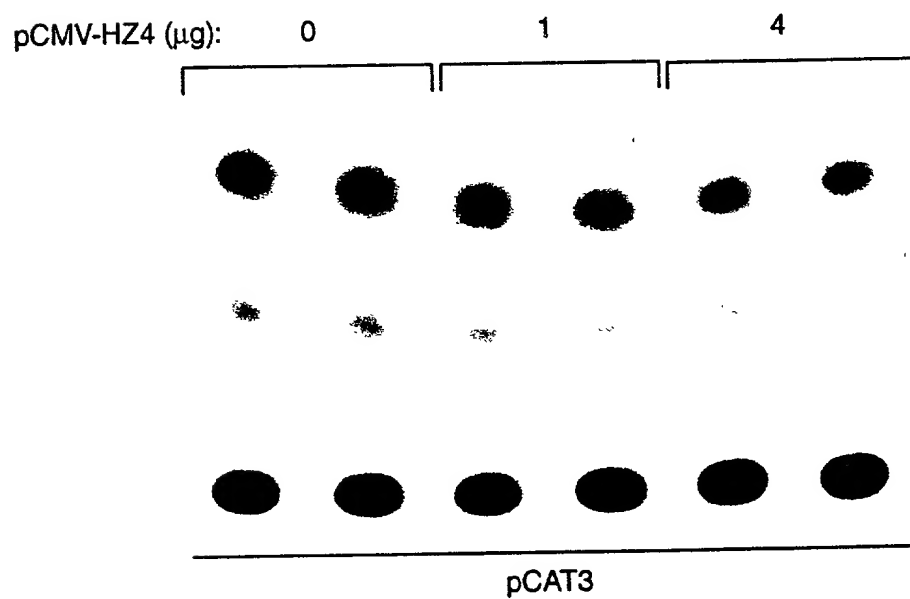


FIG. 8B

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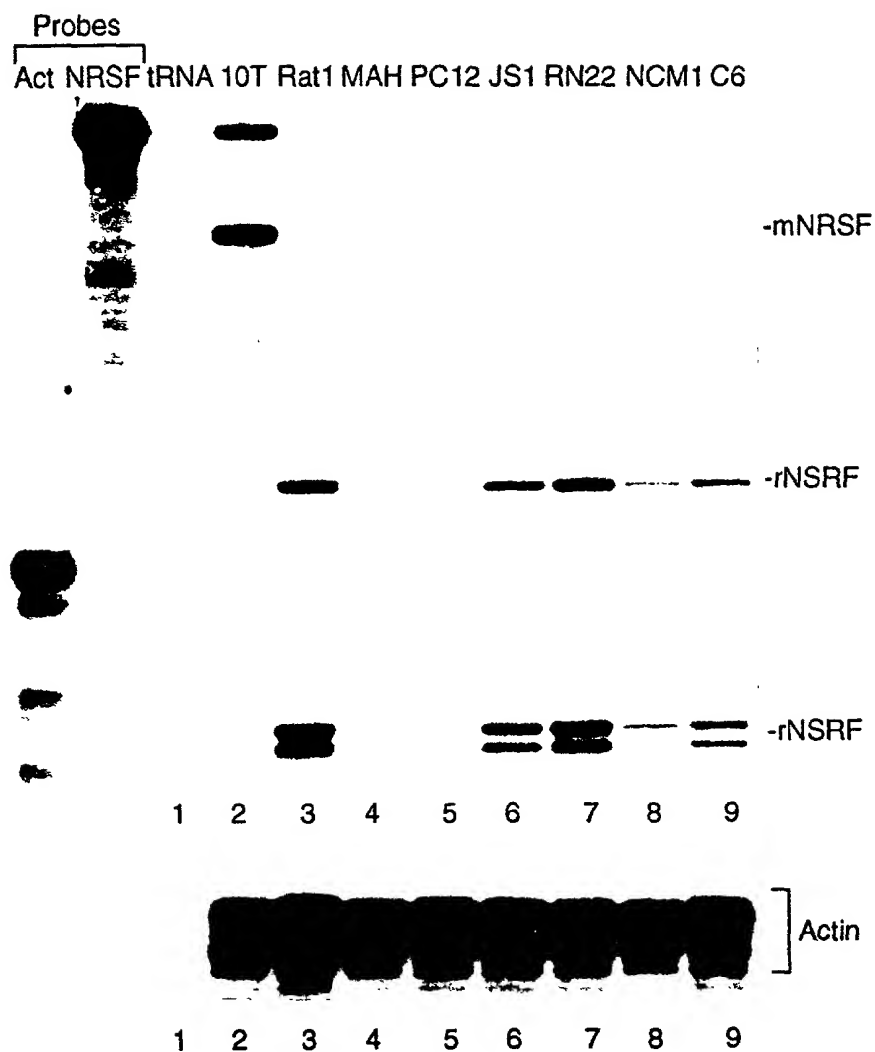


FIG._9



FIG. 10B



FIG. 10A

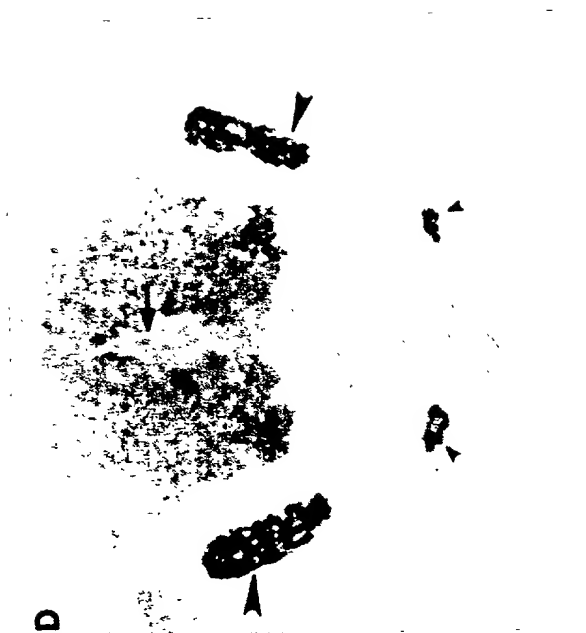


FIG. 10D

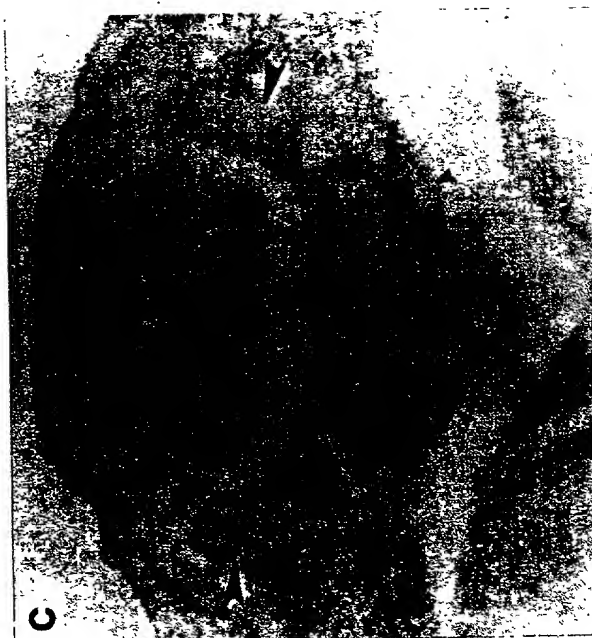


FIG. 10C

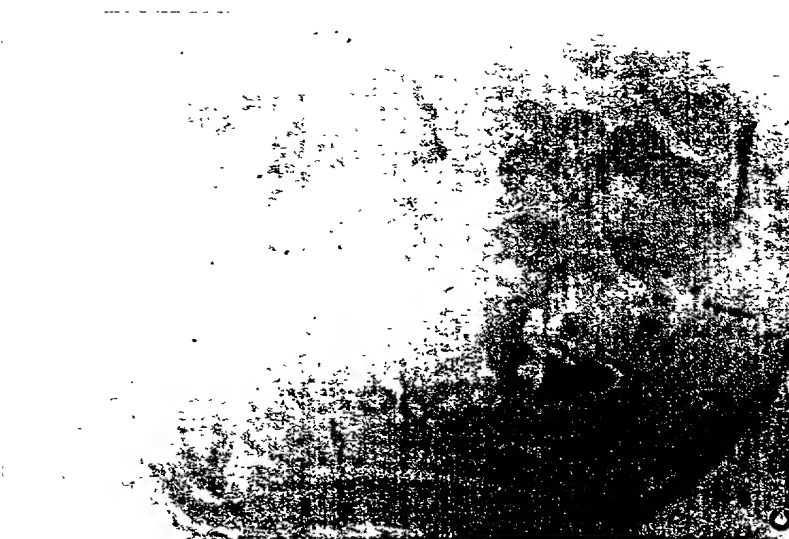


FIG. 11C



FIG. 11B



FIG. 11A

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TTCGGACGAG	GCGGGCGGGC	GGCGACGGCG	CGGGCGGGTG	CGCGGCGCAG	CGTCCTGTGC	60
TGGAATGTGC	GGCTCCCGCG	AGCTCGCGGC	GCAGCAGCAG	AAGACCGAGG	AGCGCCGCCG	120
AGGCCGCGGG	CCCCAGACCC	GGGCGGCCGG	GACCGCAGCG	ACGGCAGAAC	CAGGGCCGGC	180
GGTCTGATCC	CGCTCCGCGA	TCGCACCCCG	GGATCTCGAG	GGCCTCGACG	CCCAACTTTT	240
CCCCGCTCTC	CCTCCCCTCC	CCTCCCCCGA	AAGTCCAGCA	ACAAAGAAAA	GGAGTTGGAG	300
CGGCGRCGAC	GCGGGGGTGG	CGGACCGTGG	GCGCACAGTT	CAGAGGAGTA	CAGTT ATG	358
					Met	
					1	
GCC ACC CAG GTG ATG GGG CAG TCT TCT GGA GGA GGC AGT CTC TTC AAC						406
Ala Thr Gln Val Met Gly Gln Ser Ser Gly Gly Gly Ser Leu Phe Asn						
	5				10	15
AAC AGT GCC AAC ATG GGC ATG GSC TTA ACC AAC GAC ATG TAC GAC CTG						454
Asn Ser Ala Asn Met Gly Met Xaa Leu Thr Asn Asp Met Tyr Asp Leu						
	20				25	30
CAC GAG CTC TCG AAA GCT GAA CTG GCA GCC CCT CAG CTC ATC ATG TTA						502
His Glu Leu Ser Lys Ala Glu Leu Ala Ala Pro Gln Leu Ile Met Leu						
	35				40	45
GCC AAC GTG GCC CTG ACG GGG GAG GCA AGC GGC AGC TGC TGC GAT TAC						550
Ala Asn Val Ala Leu Thr Gly Glu Ala Ser Gly Ser Cys Cys Asp Tyr						
	50				55	60
						65
CTG GTC GGT GAA GAG AGG CAG ATG GCC GAA TTG ATG CCC GTG GGA GAC						598
Leu Val Gly Glu Glu Arg Gln Met Ala Glu Leu Met Pro Val Gly Asp						
					70	75
						80
AAC CAC TTC TCA GAA AGT GAA GGA GAA GGC CTG GAA GAG TCG GCT GAC						646
Asn His Phe Ser Glu Ser Glu Gly Glu Gly Leu Glu Glu Ser Ala Asp						
					85	90
						95
CTC AAA GGG CTG GAA AAC ATG GAA CTG GGA AGT TTG GAG CTA AGT GCT						694
Leu Lys Gly Leu Glu Asn Met Glu Leu Gly Ser Leu Glu Leu Ser Ala						
					100	105
						110
GTA GAA CCC CAG CCC GTA TTT GAA GCC TCA GCT GCC CCA GAA ATA TAC						742
Val Glu Pro Gln Pro Val Phe Glu Ala Ser Ala Ala Pro Glu Ile Tyr						
					115	120
						125
AGC GCC AAT AAA GAT CCC GCT CCA GAA ACA CCC GTG GCG GAA GAC AAA						790
Ser Ala Asn Lys Asp Pro Ala Pro Glu Thr Pro Val Ala Glu Asp Lys						
					130	135
						140
						145
TGC AGG AGT TCT AAG GCC AAG CCC TTC CGG TGT AAG CCT TGC CAG TAC						838
Cys Arg Ser Ser Lys Ala Lys Pro Phe Arg Cys Lys Pro Cys Gln Tyr						
					150	155
						160

FIG. 12A

FIG. 12A
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GAA GCC GAA TCT GAA GAG CAG TTT GTG CAT CAC ATC CGG ATT CAC AGC Glu Ala Glu Ser Glu Glu Gln Phe Val His His Ile Arg Ile His Ser	886
165 170 175	
GCT AAG AAG TTC TTT GTG GAG GAA AGT GCA GAG AAA CAG GCC AAA GCC Ala Lys Lys Phe Phe Val Glu Glu Ser Ala Glu Lys Gln Ala Lys Ala	934
180 185 190	
TGG GAG TCG GGG TCG TCT CCG GCC GAA GAG GGC GAG TTC TCC AAA GGC Trp Glu Ser Gly Ser Ser Pro Ala Glu Glu Gly Glu Phe Ser Lys Gly	982
195 200 205	
CCC ATC CGC TGT GAC CGC TGT GGC TAC AAT ACC AAC CGG TAT GAC CAC Pro Ile Arg Cys Asp Arg Cys Gly Tyr Asn Thr Asn Arg Tyr Asp His	1030
210 215 220 225	
TAC ATG GCA CAC CTG AAG CAC CAC CTG CGA GCT GGC GAG AAC GAG CGC Tyr Met Ala His Leu Lys His His Leu Arg Ala Gly Glu Asn Glu Arg	1078
230 235 240	
ATC TAC AAG TGC ATC ATC TGC ACG TAC ACG ACG GTC AGC GAG TAC CAC Ile Tyr Lys Cys Ile Ile Cys Thr Tyr Thr Thr Val Ser Glu Tyr His	1126
245 250 255	
TGG AGG AAA CAC CTG AGA AAC CAT TTC CCC AGG AAA GTC TAC ACC TGC Trp Arg Lys His Leu Arg Asn His Phe Pro Arg Lys Val Tyr Thr Cys	1174
260 265 270	
AGC AAG TGC AAC TAC TTC TCA GAC AGA AAA AAT AAC TAC GTT CAG CAC Ser Lys Cys Asn Tyr Phe Ser Asp Arg Lys Asn Asn Tyr Val Gln His	1222
275 280 285	
GTG CGA ACT CAC ACA GGA GAA CGC CCG TAT AAA TGT GAA CTT TGT CCT Val Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Glu Leu Cys Pro	1270
290 295 300 305	
TAC TCA AGC TCT CAG AAG ACT CAT CTA ACG CGA CAC ATG CGG ACT CAT Tyr Ser Ser Ser Gln Lys Thr His Leu Thr Arg His Met Arg Thr His	1318
310 315 320	
TCA GGT GAG AAG CCA TTT AAA TGT GAT GAG TGC AAT TAT GTG GCC TCT Ser Gly Glu Lys Pro Phe Lys Cys Asp Glu Cys Asn Tyr Val Ala Ser	1366
325 330 335	
AAT CAG CAT GAA GTG ACC CGA CAT GCA AGA CAG GTT CAC AAC GGG CCT Asn Gln His Glu Val Thr Arg His Ala Arg Gln Val His Asn Gly Pro	1414
340 345 350	
AAA CCT CTT AAT TGC CCG CAC TGT GAC TAC AAA ACA GCA GAT AGA AGC Lys Pro Leu Asn Cys Pro His Cys Asp Tyr Lys Thr Ala Asp Arg Ser	1462
355 360 365	
AAC TTC AAA AAG CAC GTG GAG CTG CAT GTT AAC CCA CGG CAG TTC AAC Asn Phe Lys Lys His Val Glu Leu His Val Asn Pro Arg Gln Phe Asn	1510
370 375 380 385	

FIG. 12B**SUBSTITUTE SHEET (RULE 26)**

FOI 0907552860

